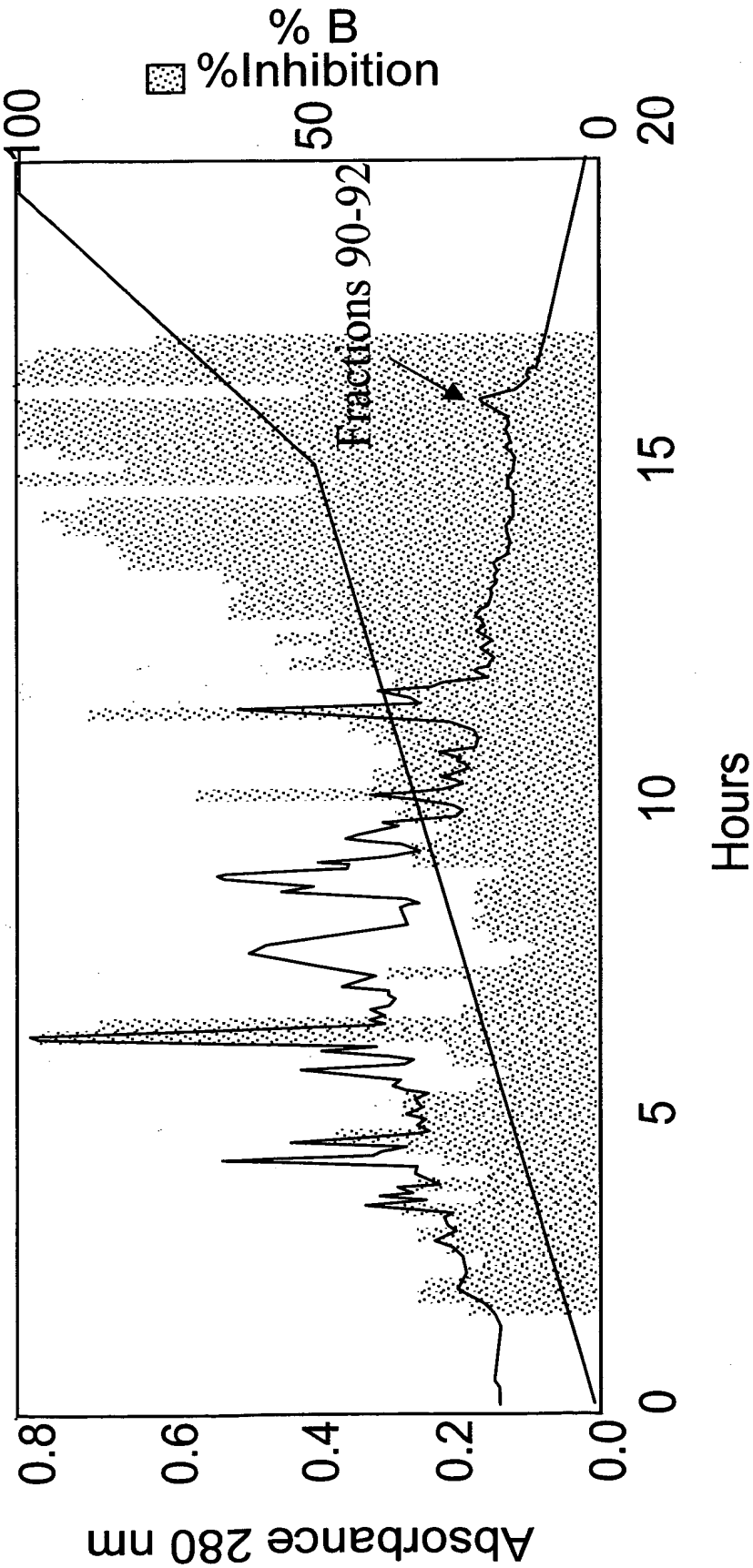


Fig. 1

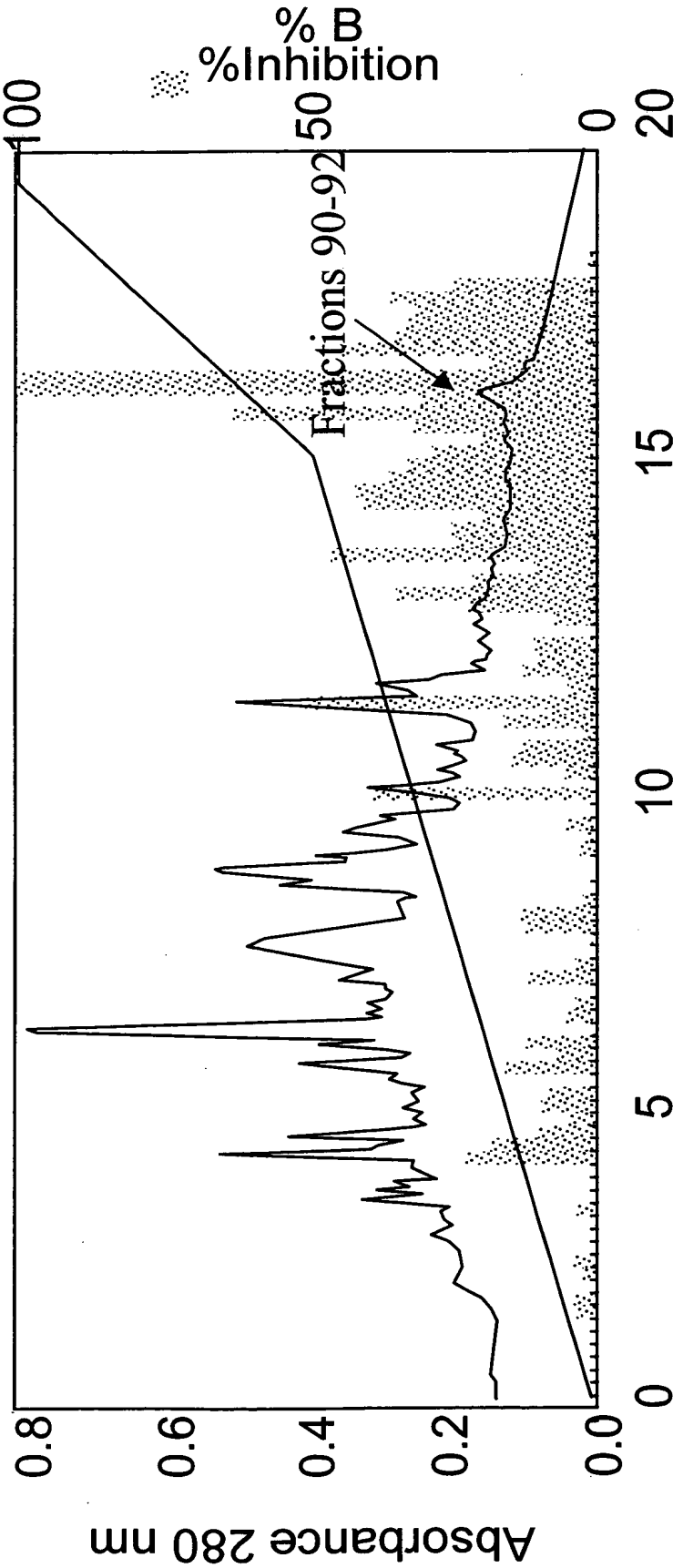

% B
%Inhibition
100
50
0
20
15
10
5
0
Hours
Fractions 90-92
0.8
0.6
0.4
0.2
0.0
Absorbance 280 nm

Fig. 2

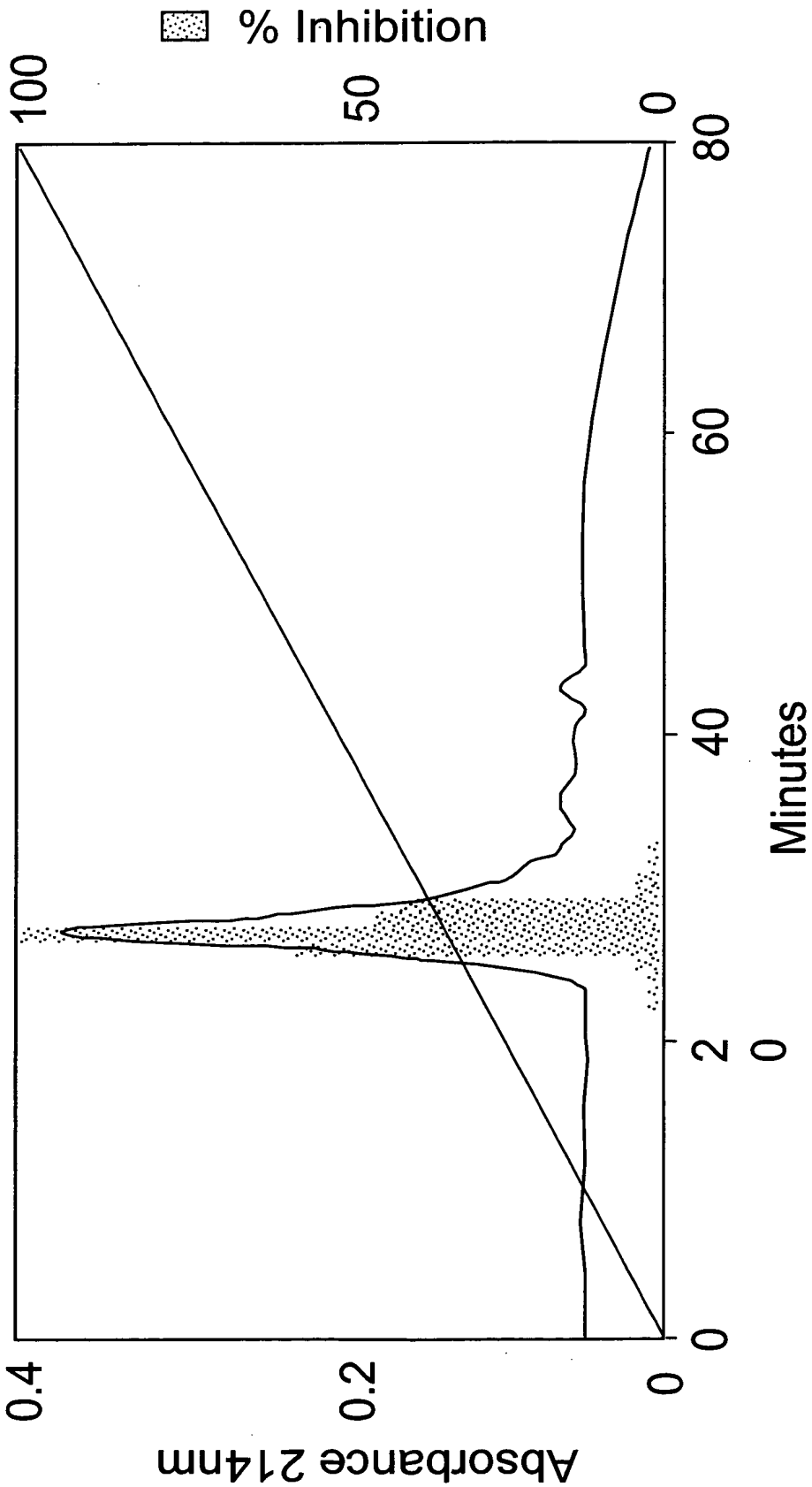

% Inhibition
100
50
0
80
60
40
20
0
Minutes
0.4
0.2
0
Absorbance 214nm

Fig. 3

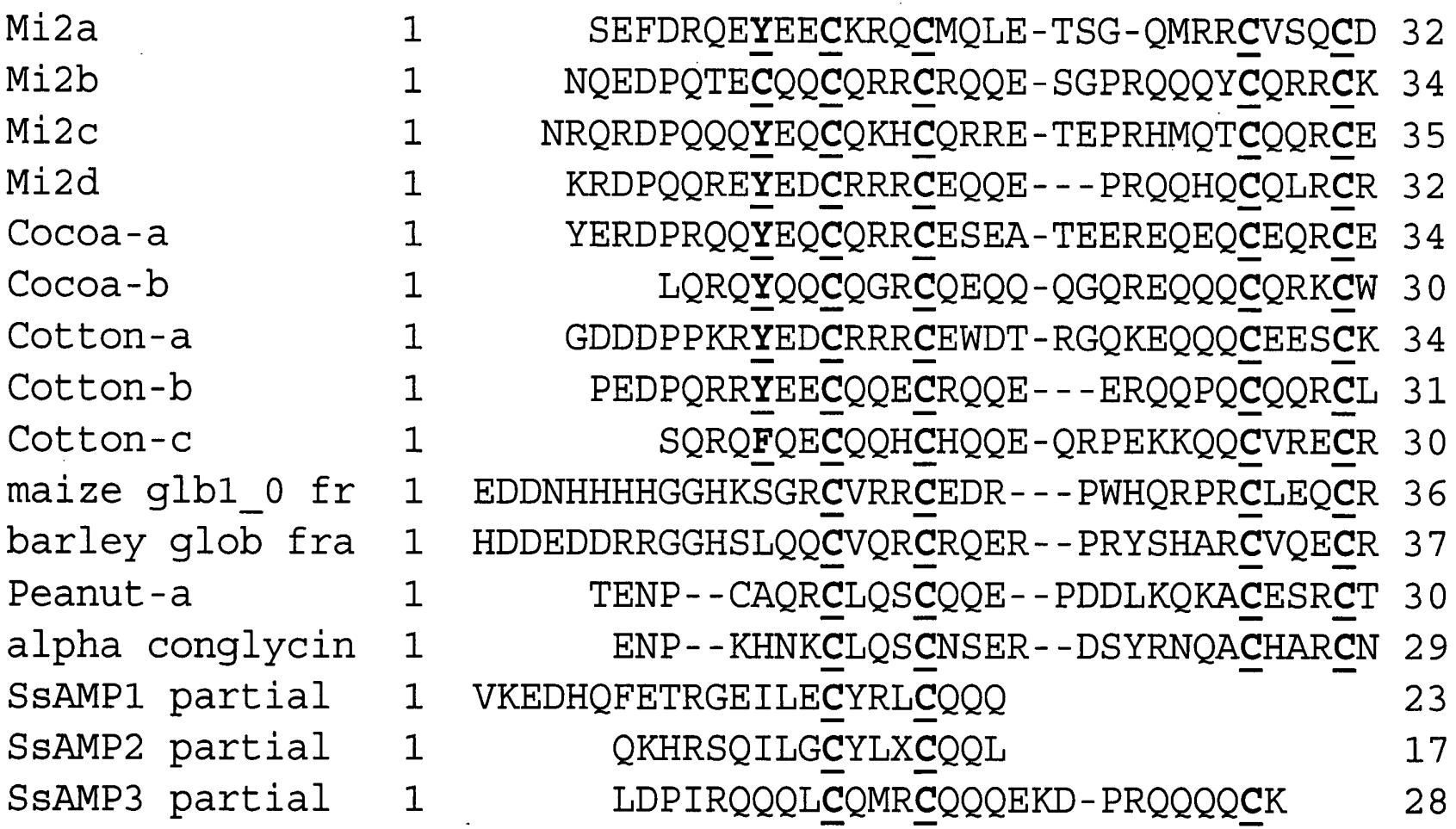

Mi2a 1 SEFDRQEYEECKRQCMQLE-TSG-QMRRCVSQCD 32
Mi2b 1 NQEDPQTECQQCQRRCRQQE-SGPRQQQYCQRRCK 34
Mi2c 1 NRQRDPQQQYEQCQKHCQRRE-TEPRHMQTCQQRCE 35
Mi2d 1 KRDPQQREYEDCRRRCEQQE---PRQQHQCQLRCR 32
Cocoa-a 1 YERDPRQQYEQCQRRCESEA-TEEREQEQCEQRCE 34
Cocoa-b 1 LQRQYQQCQGRCQEQQ-QGQREQQQCQRKCW 30
Cotton-a 1 GDDDPPKRYEDCRRRCEWDT-RGQKEQQQCEESCK 34
Cotton-b 1 PEDPQRRYEECQQECRQQE---ERQQPQCQQRCL 31
Cotton-c 1 SQRQFQECQQHCHQQE-QRPEKKQQCVRECR 30
maize glb1_0 fr 1 EDDNHHHHGGHKSGRCVRRCEDR---PWHQRPRCLEQCR 36
barley glob fra 1 HDDEDDRRGGHSLQQCVQRCRQER--PRYSHARCVQECR 37
Peanut-a 1 TENP--CAQRCLQSCQQE--PDDLKQKACESRCT 30
alpha conglycin 1 ENP--KHNKCLQSCNSER--DSYRNQACHARCN 29
SsAMP1 partial 1 VKEDHQFETRGEILECYRLCQQQ 23
SsAMP2 partial 1 QKHRSQILGCYLXCQQL 17
SsAMP3 partial 1 LDPIRQQQLCQMRCQQQEKD-PRQQQQCK 28

Fig. 4

Mi2a	33	KR**F**EEDIDWSKYD	45
Mi2b	35	EI**C**E**EEEEE**Y	43
Mi2c	36	RR**Y**EKEKRKQQKRYEEQQREDEEKYEERMK**EED**N	69
Mi2d	33	EQQRQHGRGGDMMNPQRGGSGRY**EEGEEE**QS	63
Cocoa-a	35	RE**Y**KEQQRQQ**EEE**	47
Cocoa-b	31	EQ**Y**KEQERGEHENYHNHKKNRS**EEEE**GQQR	60
Cotton-a	35	SQ**Y**GEKDQQQRHR	47
Cotton-b	32	KR**F**EQEQQQ	40
Cotton-c	31	EK**Y**QENPWRGER	42
maize glb1	37	EEEREKRQERSRHEADDRSGEGSS	60
barley glob	38	DDQQQHGRHEQEEEQGRGRGWHGEG**ER**E**E**	66
Peanut-a	31	KLEYDPR**C**VYDTGATNQRHPPGERT--RGRQP	60
alpha conglycin	30	LLKVEKEE**C**EEGEIPRPRPRPQHPER	55
SsAMP1 partial	23		23
SsAMP2 partial	17		17
SsAMP3 partial	28		28

Fig. 4 (continued)

```
AACTCTAGAG CGGCCGCGTC GACTATTTTT ACAACAATTA CCAACAACAA CAAACAACAA 60

ACAACATTAC AATTACTATT TACAATTACA GGATCCACAA CAATGGCTTG GTTCCACGTT 120
                                            M  A  W     F  H  V>

TCTGTTTGTA ACGCTGTTTT CGTTGTTATT ATTATTATTA TGCTTCTTAT GTTCGTTCCT 180
 S  V  C    N  A  V  F    V  V  I    I  I  I    M  L  L  M    F  V  P>

GTTGTTAGAG GTAGACAAAG AGATCCTCAA CAACAATACG AGCAATGTCA AAAGAGGTGT 210
 V  V  R    G  R  Q  R    D  P  Q    Q  Q  Y    E  Q  C  Q    K  R  C>
            ▲

CAAAGGAGAG AGACTGAGCC TAGACACATG CAAATTTGTC AGCAAAGGTG TGAAAGGAGG 240
 Q  R  R    E  T  E  P    R  H  M    Q  I  C    Q  Q  R  C    E  R  R>

TACGAGAAGG AGAAGAGGAA GCAACAAAAG AGGTGAGGAT CCGTCGACGC GGCCGCAGAT 270
 Y  E  K    E  K  R  K    Q  Q  K    R  *

CTAGACAA 278
```

Fig. 5

```
Mi clone 1          1   MAINTSNLCSLLFLLSL-FLLSTTVSLAE----SEFDRQEYEE  38
Mi clone 2          1   MAINTSNLCSLLFLLSL-FLLSTTVSLAE----SEFDRQEYEE  38
Mi clone 3          0                                                 0
cotton vicilin      1   MVRNKSACVVLLFSLFLSFGLLCSAKDFPGRRGDD--------  35
cocoa vicilin       1   MVISKSPFIVLIFSLLLSFALLCSGVSAYGRKQYER-------  36
                        *. . *    *.* * * *.*  ..  .

Mi clone 1         39 CKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYDNQEDPQTECQ  83
Mi clone 2         39 CKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYDNQdDPQTdCQ  83
Mi clone 3         42    QCMQLETSGQMRRCVSQCDKRFEEDIDWSKYDNQEDPQTECQ  83
cotton vicilin     36 ------------------------------------DPPKRYE  42
cocoa vicilin      37 ------------------------------------DPRQQYE  43
                                                          **    .

Mi clone 1         84 QCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQY 126
Mi clone 2         84 QCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQY 126
Mi clone 3         84 QCQRRCRQQESdPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQY 126
cotton vicilin     43 DCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRY  87
cocoa vicilin      44 QCQRRCESEATEEREQEQCEQRCEREYKEQQRQQ---EEELQRQY  85
                       *.***       ..*. *.  *     *    .     . *..*
```

Fig. 6

```
Mi clone 1      127 EQCQKhCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQRE 171
Mi clone 2      127 EQCQeRCQRhETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQRE 171
Mi clone 3      127 EQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQRE 171
cotton vicilin   88 EECQQECRQQEE--RQQPQCQQRCLKRFEQEQQ------------ 118
cocoa vicilin    86 QQCQGRCQEQQQGQREQQQCQRKCWEQY-KEQ------------ 116
                    ..**  *. ..   *    **..*  .. .*.

Mi clone 1      172 DEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQHQCQl 214
Mi clone 2      172 DEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQYQCQR 214
Mi clone 3      172 DEEKYEERMKEgDNKRDPQQREYEDCRRhCEQQE--PRlQYQCQR 214
cotton vicilin 119 ----------------QSQRQFQECQQHCHQQEQRPEKKQQCVR 146
cocoa vicilin  117 ---------------------------------------------- 116

Mi clone 1      215 RCREQQRQHGRGGDmMNPQRGGSGRYEEGEEeQSDNPYYF-DERS 258
Mi clone 2      215 RCREQQRQHGRGGDLiNPQRGGSGRYEEGEEKQSDNPYYF-DERS 258
Mi clone 3      215 RCqEQQRQHGRGGDLMNPQRGGSGRYEEGEEKQSDNPYYF-DERS 258
cotton vicilin 147 ECREKY--QENPWRGEREEEAEEEETEEGEQEQSHNPFHF-HRRS 188
cocoa vicilin  117 ---------ER-GEHENYHNHKKNRSEEEEGQQRNNPYYFPKRRS 151
                                          ** *  *  **. *   **
```

Fig. 6 (continued)

```
Mi clone 1      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVL 303
Mi clone 2      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVL 303
Mi clone 3      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVL 303
cotton vicilin 189 FQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVL 233
cocoa vicilin   152 FQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAMFEANPNTFIL 196
                     .*** * *.  .*. *     *. .  .** . *****.*.*

Mi clone 1      304 PTHLDADAILLVIGGRGALKMIHhDNRESYNLECGDVIRIPAGTT 348
Mi clone 2      304 PTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTT 348
Mi clone 3      304 PTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTT 348
cotton vicilin 234 PHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGST 278
cocoa vicilin   197 PHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGST 241
                    * * **. *  * .*.*..  . ..*.****.  * *. .***.*

Mi clone 1      349 FYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTF 393
Mi clone 2      349 FYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTF 393
Mi clone 3      349 FYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTF 393
cotton vicilin 279 VYLANQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAF 323
cocoa vicilin   242 VYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAF 286
                     *.  .** *.* **     .  **..  ***** . *. *  .*
```

Fig. 6 (continued)

```
Mi clone 1      394 SKEILEAALNTQTEkLRGVf----GQQRE-GVIIRASQEQIRELT 433
Mi clone 2      394 SKEILEAALNTQaERLRGVL----GQQRE-GVIISASQEQIRELT 433
Mi clone 3      394 SKEILEAALNTQTERLRGVL----GQQRE-GVIIRASQEQIRELT 433
cotton vicilin  324 SREILEPAFNTRSEQLDELFGGRQSRRRQQGQG-MFRKASQEQIR 367
cocoa vicilin   287 SYEVLETVFNTQREKLEEILEEQRGQKRQQGQQGMFRKAKPEQIR 331
                    * *.**   **. *.*  .      ..*. *      .    ..

Mi clone 1      434 RDDSESRhWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
Mi clone 2      434 RDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
Mi clone 3      434 RDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
cotton vicilin  368 ALSQEATSPREK-SGE--RFAFNLLSQTPRYSNQNGRFFEACPPE 409
cocoa vicilin   332 AISQQATSPRHR-GGE--RLAINLLSQSPVYSNQNGRFFEACPED 373
                      ..   . .  **  *   **  . * ***. *. .*  * .

Mi clone 1      479 YRQLQDMDlSVFIANvTQGSMMGPFFNTRSTKVVVVASGEADVEM 523
Mi clone 2      479 YRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEM 523
Mi clone 3      479 YRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEM 523
cotton vicilin  410 FRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEGNGYAEM 454
cocoa vicilin   374 FSQFQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQM 418
                    . * . . ..*    ..**..  * .*...* *. *. *    .*
```

Fig. 6 (continued)

```
Mi clone 1      524 ACPHLSGRHGGRGGGKRHEEEED-----VHYEQVRARLSKREAIV 563
Mi clone 2      524 ACPHLSGRHGGRrGGKRHEEEED-----VHYEQVkARLSKREAIV 563
Mi clone 3      524 ACPHLSGRHGGRGGGKRHEEEEE-----VHYEQVRARLSKREAIV 563
cotton vicilin 455 VSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGD 499
cocoa vicilin  419 ACPHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQVKAPLSPGD 463
                    .***   .            *.          . .   .

Mi clone 1      564 ---VLAGHPVVFVSSGNENLLLFAFGINAQNNHEN-----FLAGR 600
Mi clone 2      564 ---VpvGHPVVFVSSGNENLLLFAFGINAQNNHEN-----FLAGR 600
Mi clone 3      564 ---VLAGHPVVFVSSGNENLLLFAFGINAQNNHEN-----FLAGR 600
cotton vicilin 500 IFVVPANFPVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGK 544
cocoa vicilin  464 VFVAPAGHAVTFFASKDQPLNAVAFGLNAQN-----NQRIFLAGR 503
                        .  * * .*   . *    **.  **          *.**.

Mi clone 1     601 ERNVLQQIEPQAMELAFAAPRKEVEEsFNSQ-DqSIFFPGPRQHQQ 645
Mi clone 2     601 ERNVLQQIEPQAMELAFAAPRKEVEELFNSQ-DESIFFPGPRQHQQ 645
Mi clone 3     601 ERNVLQQIEPQAMELAFAAsRKEVEELFNSQ-DESIFFPGPRQHQQ 645
cotton vicili 545 INHVRQ-WDSQAKELAFGVSSRLVDEIFNSNPQES-YF-VSRQRQR 587
cocoa vicilin 504 --------- -------------------------PFFLNHKQNTN 514
                                                    .*   ..
```

Fig. 6 (continued)

Mi clone 1	646	QSPRSTKQQQPLVSILDFVGF	666
Mi clone 2	646	QS**s**RSTKQQQPLVSILDFVGF	666
Mi clone 3	646	QSPRSTKQQQPLVSILDFVGF	666
cotton vicilin	588	ASE	590
cocoa vicilin	515	VIKFTVKASAY	525

Fig. 6 (continued)

	1	10	20	30	40	47
MiAMP2c	**RQRDP<u>QQQYE</u>**	**<u>QCQKRCQRRE</u>**	**TEPRH<u>MQICQ</u>**	**<u>QRCERRYEKE</u>**	**<u>KRKQQKR</u>**	
Gibrat method	CCCCCCCCCH	HHECCCCCCC	CCCCCCEEEC	CCCCCCCHHH	HHHHHHH	
Levin method	CCCCCHCCHH	HHHHHHCHHT	HCSCCCCECC	CHHHTHHHHH	HHHHCHH	
DPM method	CCCCCCCCCH	HHHHHHHHHH	CHCCCHHEEH	HHHHHHHHHH	HHHHHCC	
SOPMA method	CCCCCHHHHH	HHHHHEECCC	CCCCHEEEEE	EHHHHHHHHH	HHHHHHH	
PhD method	CCCCHHHHHH	HHHHHHHHHH	CCCCCHHHHH	HHHHHHHHHH	HHHHCCC	
Consensus	CCCCC<u>HCCHH</u>	<u>HHHHHH-HH-</u>	CCCCC<u>--EE-</u>	<u>-HHHHHHHHH</u>	<u>HHHHHHH</u>	

Fig. 7

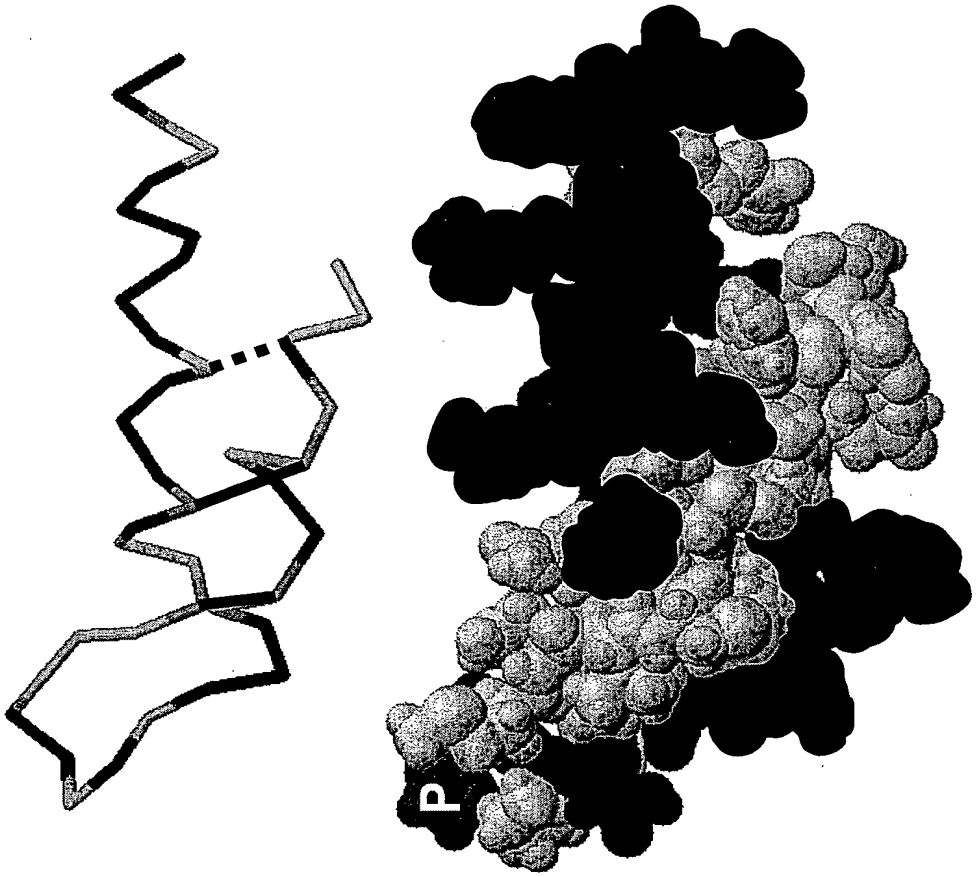


Fig. 8

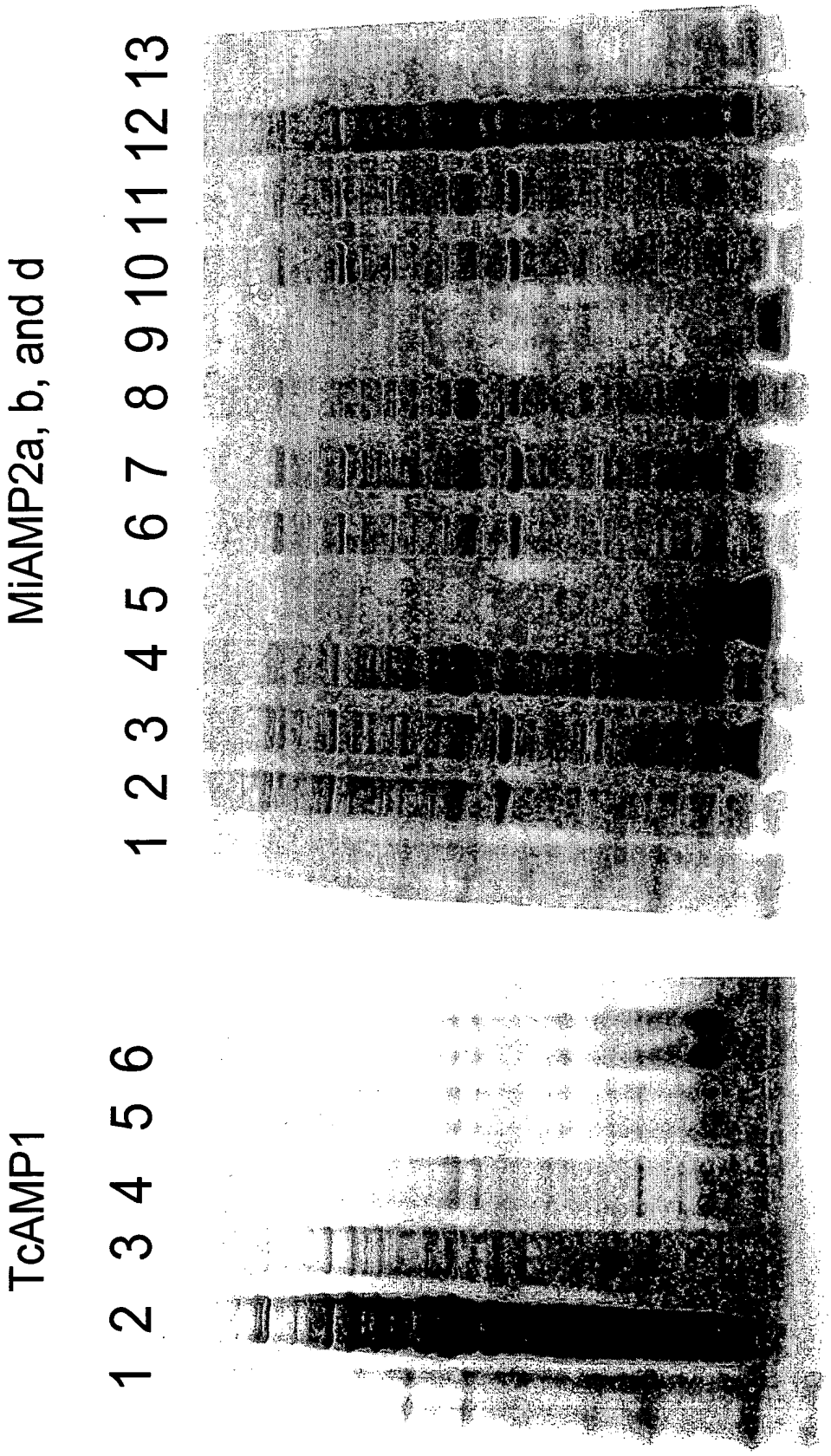


Fig. 9

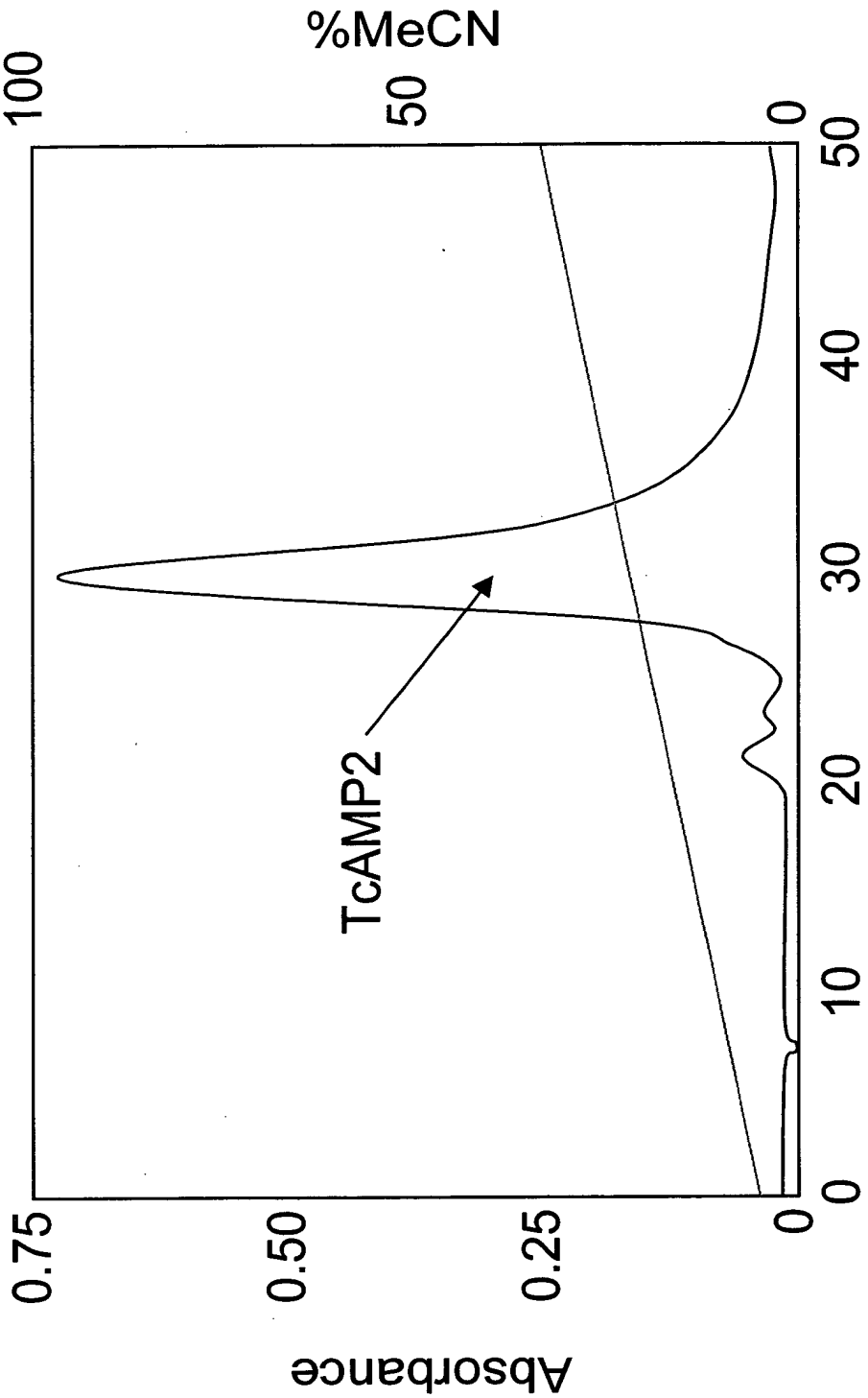

%MeCN
100
50
0
50
40
30
20
10
0
minutes
TcAMP2
0.75
0.50
0.25
0
Absorbance

Fig. 10

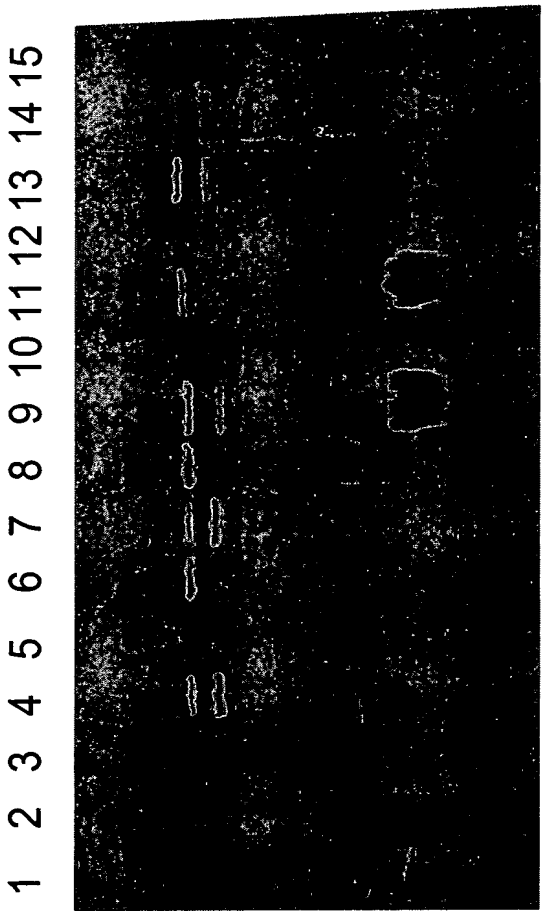


Fig. 11

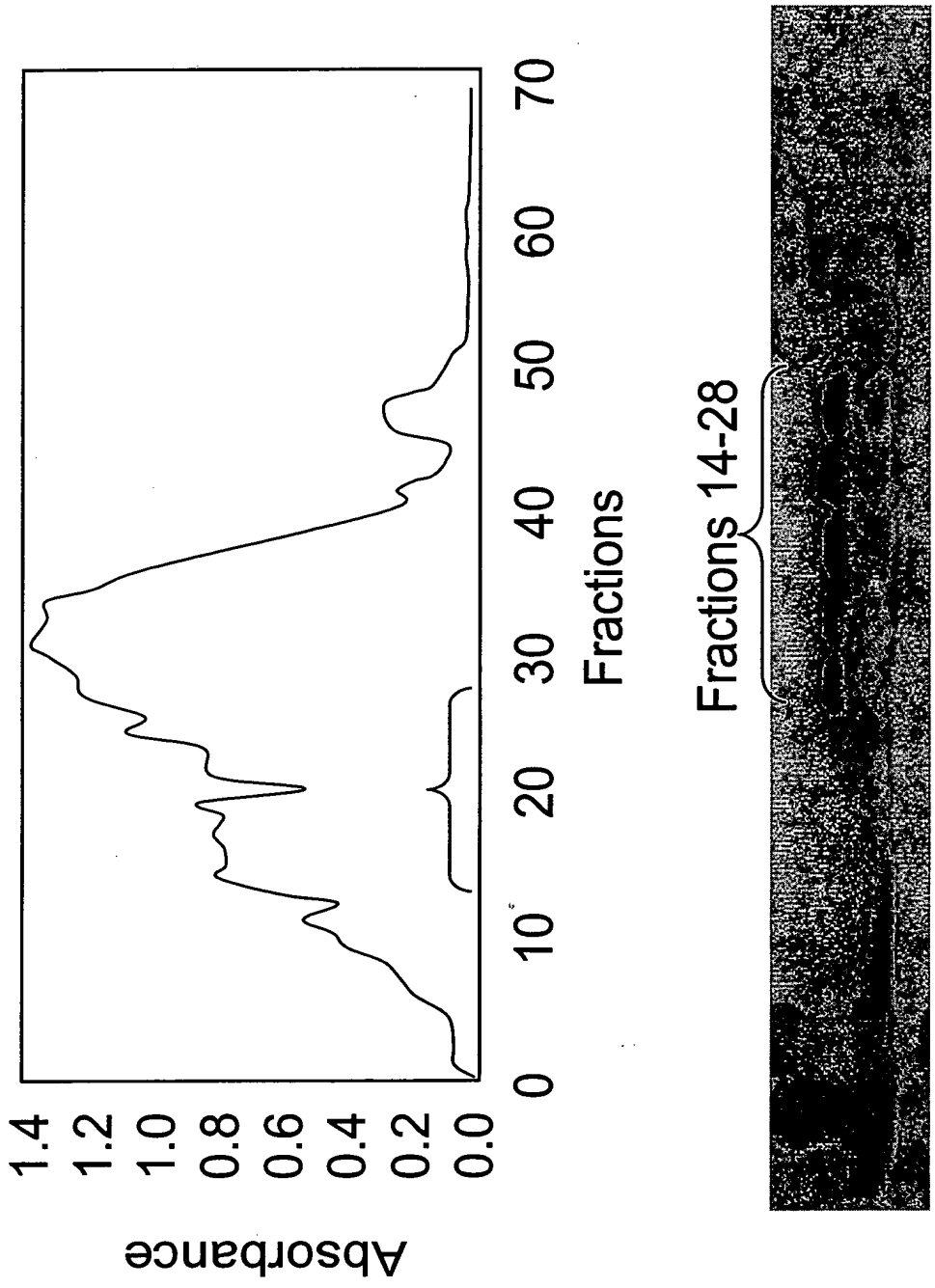
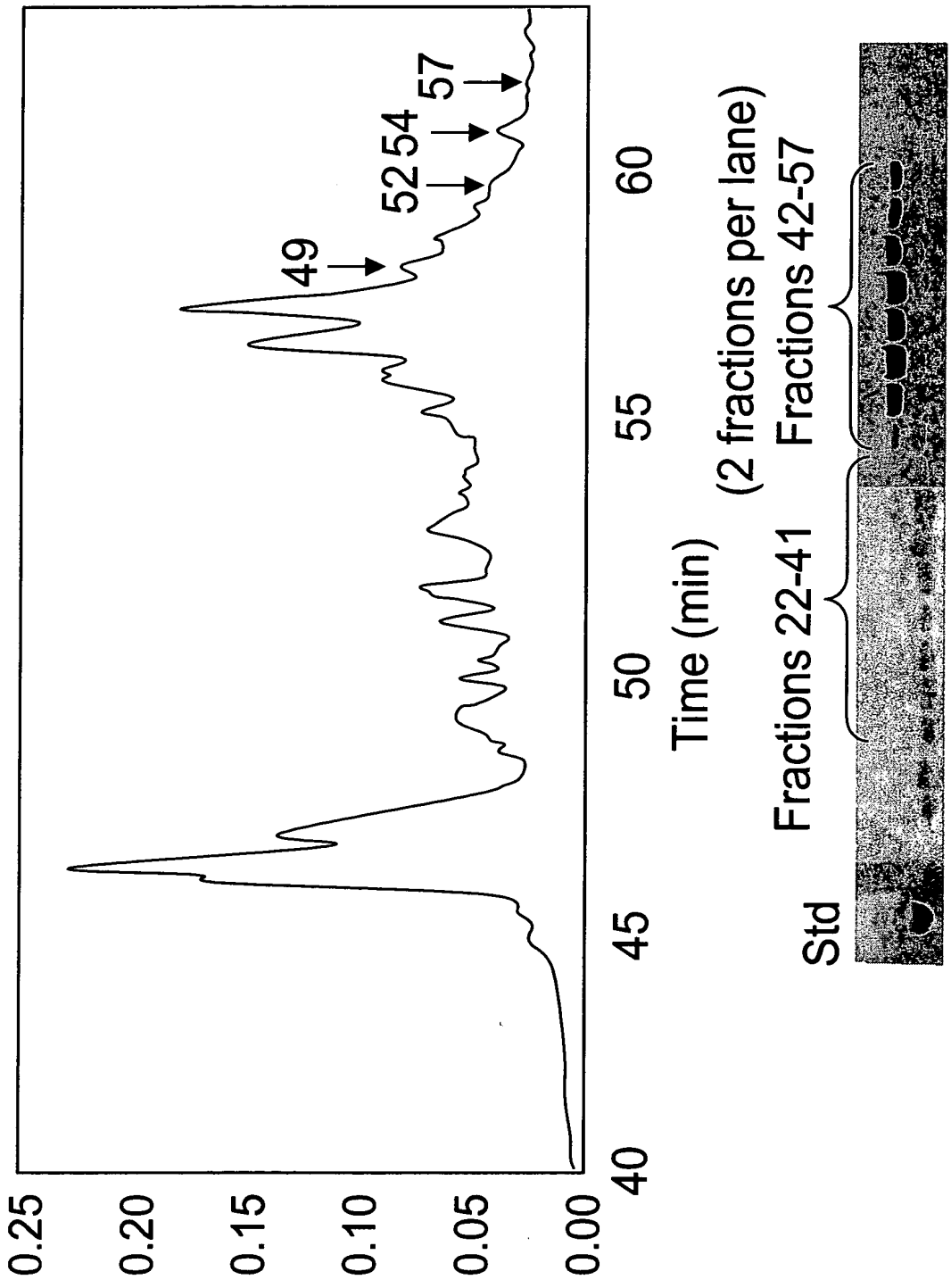

Absorbance
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
60
70
Fractions
Fractions 14-28

Fig. 12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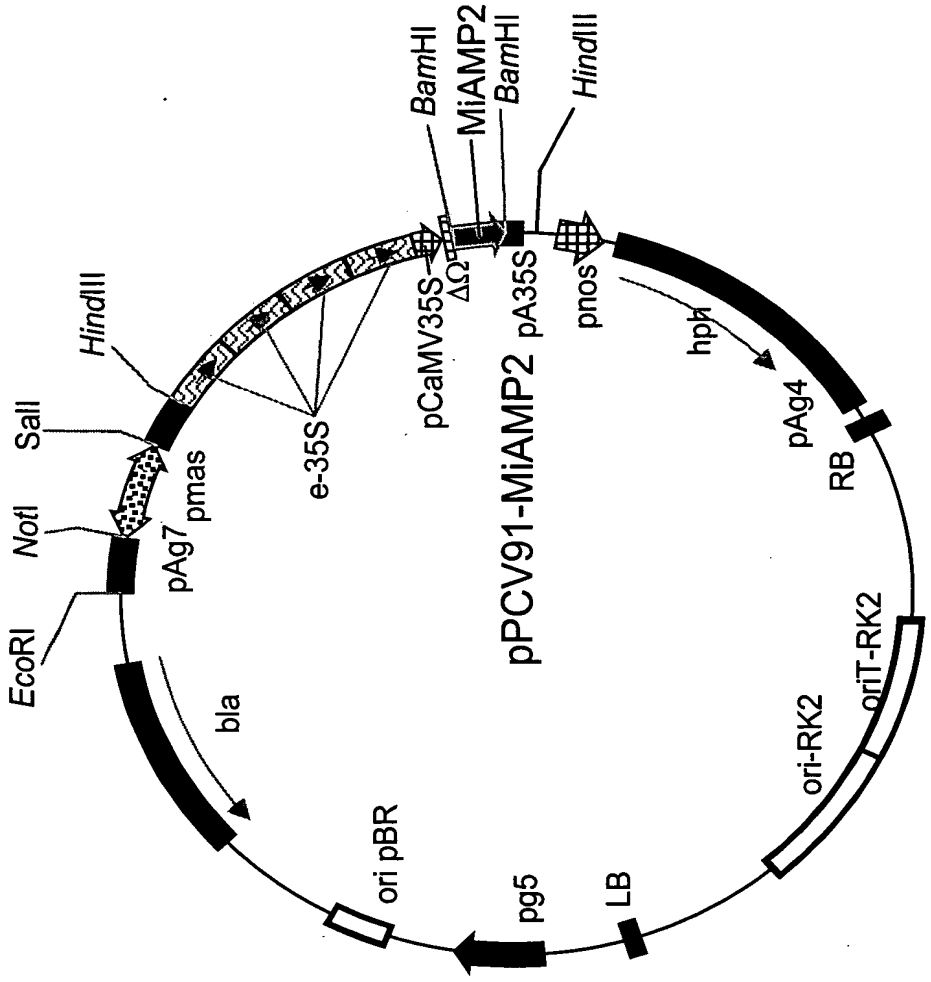
0.20
0.15
0.10
0.05
0.00
40
45
50
55
60
Time (min)
49
52
54
57
(2 fractions per lane)
Fractions 22-41
Fractions 42-57
Std

Fig. 13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BamHI
MiAMP2
BamHI
HindIII
pCaMV35S
ΔΩ
pA35S
pnos
hph
pAg4
RB
oriT-RK2
ori-RK2
LB
pg5
ori pBR
bla
pAg7
pmas
e-35S
HindIII
SalI
NotI
EcoRI

Fig. 14

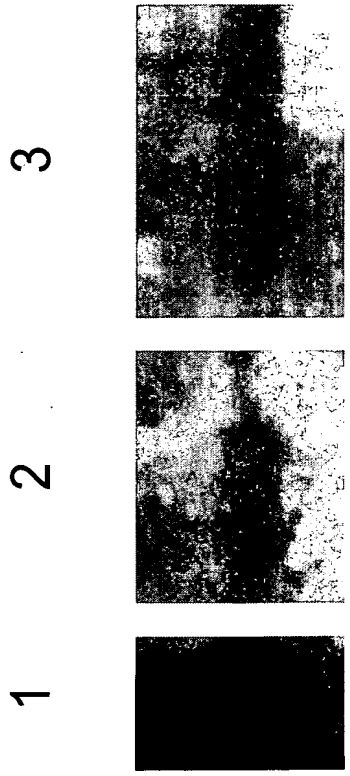

Fig. 15